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☐ 1: P77455. Reports MaoC protein (Phe...[gi:2494078]   BLink, Domains, Links

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LOCUS       P77455                   681 aa            linear   BCT 13-SEP-2005
DEFINITION  MaoC protein (Phenylacetic acid degradation protein paaZ).
ACCESSION   P77455
VERSION     P77455  GI:2494078
DBSOURCE    swissprot: locus MAOC_ECOLI, accession P77455;
            class: standard.
            extra accessions:O53009,created: Nov 1, 1997.
            sequence updated: Nov 1, 1997.
            annotation updated: Sep 13, 2005.
            xrefs: X97452.1, CAA66089.1, U00096.2, AAC74469.1, D90777.1,
            BAA14997.1, F64889
            xrefs (non-sequence databases): EchoBASEEB3498, EcoGeneEG13735,
            InterProIPR002086, InterProIPR002539, InterProIPR011966,
            PfamPF00171, PfamPF01575, TIGRFAMsTIGR02278, PROSITEPS00070,
            PROSITEPS00687
KEYWORDS    Complete proteome; Oxidoreductase.
SOURCE      Escherichia coli
  ORGANISM  Escherichia coli
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Escherichia.
REFERENCE   1  (residues 1 to 681)
  AUTHORS   Ferrandez,A., Minambres,B., Garcia,B., Olivera,E.R., Luengo,J.M.,
            Garcia,J.L. and Diaz,E.
  TITLE     Catabolism of phenylacetic acid in Escherichia coli.
            Characterization of a new aerobic hybrid pathway
  JOURNAL   J. Biol. Chem. 273 (40), 25974-25986 (1998)
   PUBMED   9748275
  REMARK    NUCLEOTIDE SEQUENCE.
            STRAIN=W / ATCC 11105
REFERENCE   2  (residues 1 to 681)
  AUTHORS   Blattner,F.R., Plunkett,G. III, Bloch,C.A., Perna,N.T., Burland,V.,
            Riley,M., Collado-Vides,J., Glasner,J.D., Rode,C.K., Mayhew,G.F.,
            Gregor,J., Davis,N.W., Kirkpatrick,H.A., Goeden,M.A., Rose,D.J.,
            Mau,B. and Shao,Y.
  TITLE     The complete genome sequence of Escherichia coli K-12
  JOURNAL   Science 277 (5331), 1453-1474 (1997)
   PUBMED   9278503
  REMARK    NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
            STRAIN=K12 / MG1655
REFERENCE   3  (residues 1 to 681)
  AUTHORS   Aiba,H., Baba,T., Fujita,K., Hayashi,K., Inada,T., Isono,K.,
            Itoh,T., Kasai,H., Kashimoto,K., Kimura,S., Kitakawa,M.,
            Kitagawa,M., Makino,K., Miki,T., Mizobuchi,K., Mori,H., Mori,T.,
            Motomura,K., Nakade,S., Nakamura,Y., Nashimoto,H., Nishio,Y.,
            Oshima,T., Saito,N., Sampei,G., Seki,Y., Sivasundaram,S.,
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                    Tagami,H., Takeda,J., Takemoto,K., Takeuchi,Y., Wada,C.,
                    Yamamoto,Y. and Horiuchi,T.
     TITLE          A 570-kb DNA sequence of the Escherichia coli K-12 genome
                    corresponding to the 28.0-40.1 min region on the linkage map
     JOURNAL        DNA Res. 3 (6), 363-377 (1996)
      PUBMED        9097039
     REMARK         NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                    STRAIN=K12
REFERENCE           4  (residues 1 to 681)
   AUTHORS          Ferrandez,A., Garcia,J.L. and Diaz,E.
   TITLE            Transcriptional regulation of the divergent paa catabolic operons
                    for phenylacetic acid degradation in Escherichia coli
   JOURNAL          J. Biol. Chem. 275 (16), 12214-12222 (2000)
    PUBMED          10766858
   REMARK           TRANSCRIPTIONAL REGULATION.
COMMENT             On May 27, 2005 this sequence version replaced gi:7466625.
                    [PATHWAY] Phenylacetic acid aerobic catabolism.
                    [INDUCTION] Activated by cAMP receptor protein (CRP) and
                    integration host factor (IHF). Inhibited by paaX.
                    [SIMILARITY] Belongs to the aldehyde dehydrogenase family.
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      301 iivpqalvna vsdalvarlq kvvvgdpaqe gvkmgalvna eqradvqekv nillaagcei
      361 rlggqadlsa agaffpptll ycpqpdetpa vhateafgpv atlmpaqnqr halqlacagg
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[Entry info] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

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Entry information

Entry name	**MAOC_ECOLI**
Primary accession number	**P77455**
Secondary accession number	O53009
Entered in Swiss-Prot in	Release 35, November 1997
Sequence was last modified in	Release 35, November 1997
Annotations were last modified in	Release 48, September 2005

Name and origin of the protein

Protein name	**MaoC protein**
Synonym	**Phenylacetic acid degradation protein paaZ**
Gene name	**Name: maoC** Synonyms: paaZ OrderedLocusNames: b1387
From	Escherichia coli [TaxID: 562]
Taxonomy	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

References

[1] NUCLEOTIDE SEQUENCE.
   STRAIN=W / ATCC 11105;
   DOI=10.1074/jbc.273.40.25974;MEDLINE=98421522;PubMed=9748275 [NCBI, ExPASy, EBI, Israel, Japan]
   Ferrandez A., Minambres B., Garcia B., Olivera E.R., Luengo J.M., Garcia J.L., Diaz E.;
   "Catabolism of phenylacetic acid in Escherichia coli. Characterization of a new aerobic hybrid pathway.";
   J. Biol. Chem. 273:25974-25986(1998).

[2] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
   STRAIN=K12 / MG1655;
   DOI=10.1126/science.277.5331.1453;MEDLINE=97426617;PubMed=9278503 [NCBI, ExPASy, EBI, Israel, Japan]
   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
   "The complete genome sequence of Escherichia coli K-12.";
   Science 277:1453-1474(1997).

[3] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
   STRAIN=K12;

MEDLINE=97251357;PubMed=9097039 [NCBI, ExPASy, EBI, Israel, Japan]
Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K.,
Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
Motomura K., Nakade S., ▓▓▓, Horiuchi T.;
"A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min
region on the linkage map.";
DNA Res. 3:363-377(1996).

[4] TRANSCRIPTIONAL REGULATION.
DOI=10.1074/jbc.275.16.12214;MEDLINE=20229831;PubMed=10766858 [NCBI, ExPASy, EBI,
Israel, Japan]
Ferrandez A., Garcia J.L., Diaz E.;
"Transcriptional regulation of the divergent paa catabolic operons for phenylacetic acid degradation
in Escherichia coli.";
J. Biol. Chem. 275:12214-12222(2000).

Comments

- *PATHWAY*: Phenylacetic acid aerobic catabolism.
- *INDUCTION*: Activated by cAMP receptor protein (CRP) and integration host factor (IHF).
  Inhibited by paaX.
- *SIMILARITY*: Belongs to the aldehyde dehydrogenase family.

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Cross-references

	X97452; CAA66089.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]
EMBL	U00096; AAC74469.1; -;	[EMBL / GenBank / DDBJ]
	Genomic_DNA.	[CoDingSequence]
	D90777; BAA14997.1; -;	[EMBL / GenBank / DDBJ]
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PIR	F64889; F64889.	
EchoBASE	EB3498; -.	
EcoGene	EG13735; maoC.	
EcoCyc	EG13735; maoC.	
CMR	P77455; b1387.	
	IPR002086; Aldehyd_dehydrog.	
	IPR002539; MaoC_dehydratas.	
InterPro	IPR011966; PaaN-DH.	
	Graphical view of domain structure.	
	PF00171; Aldedh; 1.	
Pfam	PF01575; MaoC_dehydratas; 1.	
	Pfam graphical view of domain structure.	
TIGRFAMs	TIGR02278; PaaN-DH; 1.	
PROSITE	PS00070; ALDEHYDE_DEHYDR_CYS; FALSE_NEG.	
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ProDom	[Domain structure / List of seq. sharing at least 1 domain]	
HOGENOM	[Family / Alignment / Tree]	
BLOCKS	P77455.	

ProtoNet   P77455.
ProtoMap   P77455.
PRESAGE   P77455.
DIP   P77455.
ModBase   P77455.
SWISS-
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UniRef   View cluster of proteins with at least 50% / 90% identity.

Keywords

Complete proteome; Oxidoreductase.

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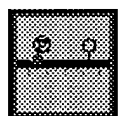
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VARIANT	440	440	1	A -> T (in strain W).
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Sequence information

Length: **681 AA**   Molecular weight: **73003 Da**   CRC64: **A631B97AA37A1C3E** [This is a checksum on the sequence]

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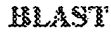
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BLAST   BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

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